M. PAK

#7200

INPUT SET: S35080.raw

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

```
1                               SEQUENCE LISTING
2
3    (1)     General Information
4
5          (i) APPLICANT: Goli, Surya K.
6                         Hillman, Jennifer L.
7                         Murry, Lynn E.
8
9         (ii) TITLE OF THE INVENTION: NOVEL HUMAN CYTOKINE/STEROID
10             RECEPTOR PROTEIN
11
12       (iii) NUMBER OF SEQUENCES: 4
13
14        (iv) CORRESPONDENCE ADDRESS:
15           (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
16           (B) STREET: 3174 Porter Drive
17           (C) CITY: Palo Alto
18           (D) STATE: CA
19           (E) COUNTRY: US
20           (F) ZIP: 94304
21
22         (v) COMPUTER READABLE FORM:
23           (A) MEDIUM TYPE: Diskette
24           (B) COMPUTER: IBM Compatible
25           (C) OPERATING SYSTEM: DOS
26           (D) SOFTWARE: FastSEQ Version 2.0
27
28        (vi) CURRENT APPLICATION DATA:
29           (A) APPLICATION NUMBER: 09/203,548
30           (B) FILING DATE:
31           (C) CLASSIFICATION:
32
33       (vii) PRIOR APPLICATION DATA:
34           (A) APPLICATION NUMBER: 08/822,264
35           (B) FILING DATE:
36
37      (viii) ATTORNEY/AGENT INFORMATION:
38           (A) NAME: Billings, Lucy J
39           (B) REGISTRATION NUMBER: 36,749
40           (C) REFERENCE/DOCKET NUMBER: PF-0233 US
41
42        (ix) TELECOMMUNICATION INFORMATION:
43           (A) TELEPHONE: 415-855-0555
44           (B) TELEFAX: 415-845-4166
45           (C) TELEX:
46
```

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RECEIVED
MAR 23 2000
TC 1600 MAIL ROOM

INPUT SET: S35080.raw

```
47
48              (2) INFORMATION FOR SEQ ID NO:1:
49
50          (i) SEQUENCE CHARACTERISTICS:
51              (A) LENGTH: 220 amino acids
52              (B) TYPE: amino acid
53              (C) STRANDEDNESS: single
54              (D) TOPOLOGY: linear
55
56          (vii) IMMEDIATE SOURCE:
57              (A) LIBRARY: CONUTUT101
58              (B) CLONE: 2504333
59
60          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
61
62  Met Ala Ala Glu Asp Val Val Ala Thr Gly Ala Asp Pro Ser Asp Leu
63   1               5               10              15
64  Glu Ser Gly Gly Leu Leu His Glu Ile Phe Thr Ser Pro Leu Asn Leu
65              20              25              30
66  Leu Leu Leu Gly Leu Cys Ile Phe Leu Leu Tyr Lys Ile Val Arg Gly
67          35              40              45
68  Asp Gln Pro Ala Ala Ser Gly Asp Arg Thr Thr Thr Xaa Pro Pro Pro
69      50              55              60
70  Leu Pro Arg Leu Lys Arg Arg Asp Phe Thr Pro Ala Glu Leu Arg Arg
71  65              70              75              80
72  Phe Asp Gly Val Gln Asp Pro Arg Ile Leu Met Ala Ile Asn Gly Lys
73              85              90              95
74  Val Phe Asp Val Thr Lys Gly Arg Lys Phe Tyr Gly Pro Glu Gly Pro
75              100             105             110
76  Tyr Gly Val Phe Ala Gly Arg Asp Ala Ser Arg Gly Leu Ala Thr Phe
77          115             120             125
78  Cys Leu Asp Lys Glu Ala Leu Lys Asp Glu Tyr Asp Asp Leu Ser Asp
79      130             135             140
80  Leu Thr Ala Ala Gln Gln Glu Thr Leu Ser Asp Trp Glu Ser Gln Phe
81  145             150             155             160
82  Thr Phe Lys Tyr His His Val Gly Lys Leu Leu Lys Glu Gly Glu Glu
83              165             170             175
84  Pro Thr Val Tyr Ser Asp Glu Glu Glu Pro Lys Asp Glu Ser Ser Arg
85              180             185             190
86  Lys Asn Val Lys Ala Phe Ser Gly Ser Ile Ser Xaa Xaa Tyr Phe Ala
87          195             200             205
88  Lys Ser Phe Val Thr Val His Xaa Val Phe Lys Thr
89      210             215             220
90
91              (2) INFORMATION FOR SEQ ID NO:2:
92
93          (i) SEQUENCE CHARACTERISTICS:
94              (A) LENGTH: 788 base pairs
95              (B) TYPE: nucleic acid
96              (C) STRANDEDNESS: single
97              (D) TOPOLOGY: linear
98
99          (vii) IMMEDIATE SOURCE:
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INPUT SET: S35080.raw

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100              (A) LIBRARY: CONUTUT101
101              (B) CLONE: 2504333
102
103          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
104
105     GCCGCCGAAC CCCGCGCGCC ACTCGCTCGC TCAGAGGGAG GAGAAAGTGG CGAGTTCCGG     60
106     ATCCCTGCCT AGCGCGGCCC AACCTTTACT CCAGAGATCA TGGCTGCCGA GGATGTGGTG    120
107     GCGACTGGCG CCGACCCAAG CGATCTGGAG AGCGGCGGGC TGCTGCATGA GATTTTCACG    180
108     TCGCCGCTCA ACCTGCTGCT GCTTGGCCTC TGCATCTTCC TGCTCTACAA GATCGTGCGC    240
109     GGGGACCAGC CGGCGGCCAG CGGCGACAGG ACGACGACGA NGCCGCCCCC TCTGCCCCGC    300
110     CTCAAGCGGC GCGACTTCAC CCCCGCCGAG CTGCGGCGCT TCGACGGCGT CCAGGACCCG    360
111     CGCATACTCA TGGCCATCAA CGGCAAGGTG TTCGATGTGA CCAAAGGCCG CAAATTCTAC    420
112     GGGCCCGAGG GGCCGTATGG GGTCTTTGCT GGAAGAGATG CATCCAGGGG CCTTGCCACA    480
113     TTTTGCCTGG ATAAGGAAGC ACTGAAGGAT GAGTACGATG ACCTTTCTGA CCTCACTGCT    540
114     GCCCAGCAGG AGACTCTGAG TGACTGGGAG TCTCAGTTCA CTTTCAAGTA TCATCACGTG    600
115     GGCAAACTGC TGAAGGAGGG GGAGGAGCCC ACTGTGTACT CAGATGAGGA AGAACCAAAA    660
116     GATGAGAGTT CCCGGAAAAA TGTTAAAGCA TTCAGTGGAA GTATATCTAT NNTGTATTTT    720
117     GCAAAATCAT TTGTAACAGT CCACTNTGTC TTTAAAACAT AGTGTTACAA TATTTAGAAA    780
118     GTTTGAGC                                                             788
119
120              (2) INFORMATION FOR SEQ ID NO:3:
121
122          (i) SEQUENCE CHARACTERISTICS:
123              (A) LENGTH: 223 amino acids
124              (B) TYPE: amino acid
125              (C) STRANDEDNESS: single
126              (D) TOPOLOGY: linear
127
128          (vii) IMMEDIATE SOURCE:
129              (A) LIBRARY: GenBank
130              (B) CLONE: 158818
131
132          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
133
134     Met Ala Ala Glu Asp Val Val Ala Thr Gly Ala Asp Pro Ser Glu Leu
135      1               5                  10                  15
136     Glu Gly Gly Gly Leu Leu Gln Glu Ile Phe Thr Ser Pro Leu Asn Leu
137                 20                  25                  30
138     Leu Leu Leu Gly Leu Cys Ile Phe Leu Leu Tyr Lys Ile Val Arg Gly
139                 35                  40                  45
140     Asp Gln Pro Gly Ala Ser Gly Asp Asn Asp Asp Asp Glu Pro Pro Pro
141         50                  55                  60
142     Leu Pro Arg Leu Lys Pro Arg Asp Phe Thr Pro Ala Glu Leu Arg Arg
143     65                  70                  75                  80
144     Tyr Asp Gly Val Gln Asp Pro Arg Ile Leu Met Ala Ile Asn Gly Lys
145                     85                  90                  95
146     Val Phe Asp Val Thr Lys Gly Arg Lys Phe Tyr Gly Pro Glu Gly Pro
147                 100                 105                 110
148     Tyr Gly Val Phe Ala Gly Arg Asp Ala Ser Arg Gly Leu Ala Thr Phe
149                 115                 120                 125
150     Cys Leu Asp Lys Glu Ala Leu Lys Asp Glu Tyr Asp Asp Leu Ser Asp
151         130                 135                 140
152     Leu Thr Pro Ala Gln Gln Glu Thr Leu Asn Asp Trp Asp Ser Gln Phe
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INPUT SET: S35080.raw

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153        145                   150                   155                   160
154        Ser Ser Pro Ser Ser Thr Ile Thr Trp Gly Lys Leu Leu Glu Gly Ala
155                            165                   170                   175
156        Glu Glu Pro Ile Val Tyr Ser Asp Asp Glu Glu Gln Lys Met Arg Leu
157                            180                   185                   190
158        Leu Gly Arg Val Thr Glu Ala Val Ser Gly Ala Tyr Leu Phe Leu Tyr
159                 195                   200                   205
160        Phe Ala Lys Ser Phe Val Thr Phe Gln Ser Val Phe Thr Thr Trp
161             210                   215                   220
162
163                  (2) INFORMATION FOR SEQ ID NO:4:
164
165             (i) SEQUENCE CHARACTERISTICS:
166                 (A) LENGTH: 194 amino acids
167                 (B) TYPE: amino acid
168                 (C) STRANDEDNESS: single
169                 (D) TOPOLOGY: linear
170
171             (vii) IMMEDIATE SOURCE:
172                 (A) LIBRARY: GenBank
173                 (B) CLONE: 1657409
174
175             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
176
177        Met Ala Ala Glu Asp Val Ala Ala Thr Gly Ala Asp Pro Ser Glu Leu
178         1                   5                   10                  15
179        Glu Gly Gly Gly Leu Leu His Glu Ile Phe Thr Ser Pro Leu Asn Leu
180                            20                  25                  30
181        Leu Leu Leu Gly Leu Cys Ile Phe Leu Leu Tyr Lys Ile Val Arg Gly
182                 35                  40                  45
183        Asp Gln Pro Ala Ala Ser Asp Ser Asp Asp Asp Glu Pro Pro Pro Leu
184              50                  55                  60
185        Pro Arg Leu Lys Arg Arg Asp Phe Thr Pro Ala Glu Leu Arg Arg Phe
186         65                  70                  75                  80
187        Asp Gly Val Gln Asp Pro Arg Ile Leu Met Ala Ile Asn Gly Lys Val
188                            85                  90                  95
189        Phe Asp Val Thr Lys Gly Arg Lys Phe Tyr Gly Pro Glu Gly Pro Tyr
190                 100                 105                 110
191        Gly Val Phe Ala Gly Arg Asp Ala Ser Arg Gly Leu Ala Thr Phe Cys
192              115                 120                 125
193        Leu Asp Lys Glu Ala Leu Lys Asp Glu Tyr Asp Asp Leu Ser Asp Leu
194              130                 135                 140
195        Thr Pro Ala Gln Gln Glu Thr Leu Asn Asp Trp Asp Ser Gln Phe Thr
196         145                 150                 155                 160
197        Phe Lys Tyr His His Val Gly Lys Leu Leu Lys Glu Gly Glu Glu Pro
198                            165                 170                 175
199        Thr Val Tyr Ser Asp Glu Glu Glu Pro Lys Asp Glu Ser Ala Arg Lys
200                 180                 185                 190
201        Asn Asp
202
203
```

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/09/203,548*

INPUT SET: S35080.raw

Line   Error   Original Text